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Copyright (c) 1993 - 2004 Compugen Ltd
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Aa655798 cochlodin
Aa655800 azeca goo
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Aa655802 columella
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ID 0921G7
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DT 01-MAY-1999 (TrEMBLrel. 10, Created)
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Brandt W.F., Strickland W.N., Morgan M., Von "Comparison of the N-terminal amino acid seque a mammal, a bird, a shark, an echinoderm, a merk factor of the N-terminal amino acid seque FEBS Lett. 40:167-172 (1974).

PERS Lett. 40:167-172 (1974).

PERS Lett. 40:167-172 (1974).

PERS Lett. 40:167-172 (1974).

PERS Lett. 40:167-172 (1974).

GO; GO:000786; C:nucleosome; IEA.
GO; GO:0005634; C:nucleosome; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003673; P:nucleosome assembly; IEA.

PRINTS; PRO0622; HISTONEH3.

PRINTS; PRO0622; HISTONEH3.
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Artishevsky A., Wooden S., Sharma A., Resende "Cell-Cycle regulatory sequences in a hamster their interactions with cellular factors.";
Mature 328:823-827(1987)

AAA42371.;
GO; GO:000786; C:nucleoseme; IEA.
GO; GO:0005634; C:nucleoseme; IEA.
GO; GO:0005634; C:nucleoseme organization and GO; GO:0003677; F:DNA binding; IEA.
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
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Name=H3.2;
Cricetulus sp.
Eukaryota; Metazoa; (
Mammalia; Eutheria; )
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"Comparison of the N-terminal amino acid sequences of histor
T a mammal, a bird, a shark, an echinoderm, a mollusc and a pl
FEBS Lett. 40:167-172(1974).
R PIR; CG1286; CG1286; C:nucleosome; IEA.
GO; GO:0000786; C:nucleosome; IEA.
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G0; G0:0007001; P:chromosome organization and
G0; G0:0006334; P:nucleosome assembly; IEA.
InterPro; IPR00614; Histone H3.
PRINTS; PR00622; HISTONEH3.
PROSITE; P800322; HISTONEH3.
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01-MAR-2004
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Encephalartos caffer (Kaffir bread).
Encephalartos caffer (Kaffir bread).
Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Cycadales; Zycadophyta; Cycadales; Zy
                                                                                                                                                                                                                                                             SEQUENCE.
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Patella granatina (Sandpaper limpet).
Eukaryota; Metazoa; Mollusca; Gastropoda; Eo
Patellina; Patelloidea; Patellidae; Patella.
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                                                         PRINTS; F
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Vallonia pulchella.
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata;
Orthurethra; Pupilloidea; Valloniidae; Vallonia.
NCBI TaxID=229284;
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AYSS9166; AASSS832.1; -.
InterPro; IPR009072; Histone-fold.
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PROSITE; PS00322; HISTONEH3.1; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                         Orthurethra; Pupilloidea;
NCBI_TaxID=145157;
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Q6Q4V8;
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Q6Q4V2;
05-UUL-2004 (TrEMBLrel. 27, C
05-UUL-2004 (TrEMBLrel. 27, L
05-UUL-2004 (TrEMBLrel. 27, L
                                                                                                                                                                                                                                                                                                      Armbruster G., Boehme M., Bernhard D., Schlegel M., Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AYS59163; AAS55826.1; ... InterPro; IPR009072; Histone-fold. InterPro; IPR009072; Histone-H3. PRUNTS; PR00622; HISTONEH3. PRUNTS; PR00522; HISTONEH3. PROSITE; PS00322; HISTONEH3_1; UNKNOWN_1.
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Q604V0;
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Acanthinula aculeata,
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Orthurethra; Pupilloidea; Valloniidae; Acanthinula.
NCBI_TaxID=229287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Armbruster G., Boehme M., Bernhard D., Sch
Submitted (FEB-2004) to the EMBL/GenBank/D
EMBL; AY559164; AA555828.1;
InterPro; IPR009072; Histone-Fold.
InterPro; IPR000164; Histone-H3.
PRINTS; PR00622; HISTONE-H3.1; UNKNOWN_1.
NON_TER 50 50
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Ena montana.

Eukaryota; Metazoa; Mollusca;

Sigmurethra; Enoidea; Enidae;

NCBI_TaxID=265227;
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                                                 PRELIMINARY;
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Pred. No. 1.3e-12;
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EMBL/GenBank/DDBJ databases.
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Pred. No. 1.3e-12;
Mismatches 0;
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(Fragment)
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A Armbrister G., Boehme M., Bernhard D., Schlegel M.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
R EMBL, AV559161; AAS55820.1; ...
R EMBL; AV559162; AAS55824.1; ...
R InterPro; IPR0009072; Histone-fold.
R InterPro; IPR000164; Histone-H3.
R InterPro, IPR0002164; Histone-H3.
R PRINTS; PR00622; HISTONEH3.
R PROSITE; PS00322; HISTONEH3.1; UNKNOWN_1.
SEQUENCE 50 AA; 5343 MW; 541518B31D426E5D CRC64;
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Q6Q4W2;
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O5-JUL-2004 (TREMBLrel. 2
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Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY559158; AAS55816.1; .
EMBL; AY559159; AAS55818.1; .
InterPro; IPR009072; Histone-fold.
InterPro; IPR009164; Histone-H3.
PRINTS; PR00622; HISTONEH3.
PROSITE; PS00322; HISTONEH3.
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50 AA; 5343 MW; 541518B31D426E5D CRC64;
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Orthurethra; Cochlicopoidea; (
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Vertigo antivertigo.
Vertigo antivertigo.
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Orthurethra; Pupilloidea; Vertiginidae; Vertigo.
NCBL_TaxID=145162;
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Pred. No. 1.3e-12;
Mismatches 0;
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Cochlicopidae; Cochlicopa
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Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Orthurethra; Cochlicopoidea; Cochlicopidae; Cochlicopa.
NCBI_TaxID=82566;
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SEQUENCE
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY559156; AAS55812.1; -.
InterPro; IPR009072; Histone-fold.
InterPro; IPR000164; Histone H3.
PRINTS; PR00622; HISTONEH3.
PROSTTE; PS00322; HISTONEH3.1; UNKNOWN_1.
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Cochlicopa nitens.
Cochlicopa nitens.
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Orthurethra; Cochlicopoidea; Cochlicopidae; Cochlicopa.
NCBI_TaxID=82568;
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                                                                                                                                                                          ch 100.0%; Score 146; DB 2; Length 50; Similarity 100.0%; Pred. No. 1.3e-12; 30; Conservative 0; Mismatches 0; Indels
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Maximum Match 100%
Listing first 45 summaries
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-248-796A-18649
US-09-451-034-13
US-09-451-034-8
US-09-451-034-8
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US-09-451-034-7
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US-08-363-255-14
US-08-363-255-14
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Sequence 7473, Ap
Sequence 5370, Ap
Sequence 1029, Ap
Sequence 1029, Ap
Sequence 13, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 39947, A
Sequence 14, Appli
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Sequence 28, Appli
Sequence 3, Appli
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Sequence 4, Appli
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Sequence 11, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 23987, A
Sequence 23987, A
Sequence 23987, A
Sequence 23987, A
Sequence 201, Appli
Sequence 201, Appli
Sequence 23987, A
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NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 7473

LENGTH: 72

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: UNSURE
LOCATION: 72

OTHER INFORMATION: Xaa = Gly, Arg, Trp
US-09-621-976-7473

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51 34.9 236 4 US-09-252-991A-18461 51 34.9 310 1 US-08-363-255-6 51 34.9 445 1 US-08-363-255-5 51 34.9 445 1 US-08-363-255-12 50.5 34.6 783 4 US-09-252-991A-17935 50 34.2 144 4 US-09-252-991A-28630 50 34.2 191 4 US-10-10-146A-753 50 34.2 191 4 US-10-9-252-991A-28630 50 34.2 191 4 US-09-252-991A-28630 50 34.2 191 4 US-09-252-991A-28630 49.5 33.9 100 4 US-09-252-991A-28630 49.5 33.9 100 4 US-09-252-991A-20892 49.5 33.9 100 4 US-09-252-991A-20892 49 33.6 269 4 US-09-252-991A-31473 49 33.6 269 4 US-09-252-991A-31473 49 33.6 269 4 US-09-252-991A-31473 49 33.6 507 4 US-09-252-991A-31473 49 33.6 1788 2 US-08-252-991A-289 49 33.6 1788 2 US-08-252-991A-17546	45	44	43	42	41	40	39	38	37	36	u S	34	ω ω	32	31	30	29	0
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	17546, A	2, Appli	289, App	31473, P	6, Appli	3, Appli	20892, A	6834, Ap	24009, A	28630, A	753, App	17329, A	18035, A	12, Appl	5, Appli	6, Appli	18461, A	1000

## ALIGNMENTS

US-09-621-976-7473

Sequence 7473, Application US/09621976 Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: JOBERT, S.
APPLICANT: Giordano, J.Y.
TIFLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21

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US-09-513-999C-5370
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                                                         TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961
PATENT REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
                                                                                                                                                                                                                                                GENERAL INFORMATION:
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Best Local Similarity
Matches 30; Conserva
                                                                                                                                                                                                                                                               Sequence 5370, Application US/09513999C Patent No. 6783961
                                                                                                                                                                                  APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
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SEQ ID NO 5370

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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
ITILE OF INVENTION. ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILIN DAYE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 7472
LENGTH. 112
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US-09-976-594-1029
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                                                                                                                                    Sequence 1029, Application US/09976594
Patent No. 6673549
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US-09-621-976-7472
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NAME/KEY: UNSURE
LOCATION: 99
OTHER INFORMATION: Xaa=Ala or Leu or Ser or Val
US-09-513-999C-5370
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Patent No. 6639063
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Best Local (
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NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                          LOCATION: 89
OTHER INFORMATION:
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ORGANISM: Homo sapiens
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ilarity 100.0%;
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Pred. No. 5.3e-14;
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CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18649
LENGTH: 152
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-18649
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-09-451-034-13
                                                                                                                                                                GENERAL INFORMATION: INHIBITORS OF HISTONE ACETYLTRANSFERASE (HATS) AND USES TITLE OF INVENTION: INHIBITORS OF HISTONE ACETYLTRANSFERASE (HATS) AND USES FILE REFERENCE: 600-1-265
CURRENT APPLICATION NUMBER: US/09/451,034
CURRENT FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 14
SOCTWARE: Patentin Ver. 2.0
SEQ ID NO 13
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Patent No. 6369030
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LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
OTHER INFORMATION: MOLECULE THAT ACT AS ENZYME INHIBITOR
OTHER INFORMATION: The A in position 1 is a modified residue and
OTHER INFORMATION: aceylated. The K in position 4 is a modified
OTHER INFORMATION: residue and is conjugated via its epsilon NH2
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Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PERL Program SEQ ID NO 1029
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NAME/KEY: misc
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Pred. No. 2.9e-13;
"'amatches 0;
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Pred. No. 6.8e-14;
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APPLICANT: Jenuwein, Thomas
APPLICANT: Rea, Stephen
APPLICANT: Rea, Stephen
APPLICANT: Cisenheber, Frank
APPLICANT: O'Carroll, Donal
ITITLE OF INVENTION: Method for identifying compounds altering higher-order chromatin
ITITLE OF INVENTION: dependent chromosome stability
FILE REFERENCE: 0652.2240001
CURRENT APPLICATION NUMBER: US/09/876,221
CURRENT APPLICATION NUMBER: EP 00 112 345.4
PRIOR APPLICATION NUMBER: EP 00 112 345.4
PRIOR APPLICATION NUMBER: EP 00 112 349.1
PRIOR APPLICATION NUMBER: EP 00 112 479.1
PRIOR APPLICATION NUMBER: US 60/224,220
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-08-09
PRIOR FILING DATE: 2000-08-09
PRIOR FILING DATE: 2000-08-09
PRIOR FILING DATE: 2000-08-09
SOFTWARE: Patentin Ver. 2.1
CURRENT APPLICATION NUMBER: US/09/589,892B
CURRENT FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: US 08/945,988
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: PCT/EP96/01818
PRIOR FILING DATE: 1996-05-02
PRIOR APPLICATION NUMBER: DE 195 16 776.7
PRIOR APPLICATION NUMBER: DE 195 16 776.7
PRIOR PILING DATE: 1995-05-10
NUMBER: DE 195 10 776.7
PRIOR PILING DATE: 1995-05-10
NUMBER: Patentin version 3.2
SEQ ID NO 19
LENGTH: 20
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; Sequence 19, Application US/09589892B
; Patent No. 6689583
; GENERAL INFORMATION:
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Best Local Similarity
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jenuwein, APPLICANT: Laible,
                                                                                                                                                                                                                                                                          APPLICANT: Rea, Stephen
TITLE OF INVENTION: Chromatin-Regulator Genes
FILE REFERENCE; 0652.1670001
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
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Eisenhaber, Frank
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100.0%; Pred. No.
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US-09-451-034-8
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; ORGANISM: Homo
US-09-589-8928-19
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                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Preventior
TITLE OF INVENTION: Microbial UC pANCA at
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, St
                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 603386
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CO1e, Philip et al TITLE OF INVENTION: INHIBITORS OF HISTONE ACETYLTRANSFERASE (HATS) AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: 600-1-265 OF CURRENT APPLICATION NUMBER: US/09/451,034 CURRENT FILING DATE: 1999-11-29 NUMBER OF SEQ ID NOS: 14
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: PART OF OTHER INFORMATION: SYNTHETIC MOLECULES THAT ACT AS ENZYME INHIOTHER INFORMATION: The first ala is a modified residue; it is OTHER INFORMATION: acetylated.
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                           STREET: 43. STREET: 43. CITY: San Diego CITY: California
                                                  SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                   Diagnosis, Prevention and Treatment of Ulcerative Colitis, and Clinical Subtypes Thereof, Using Microbial UC panCA antigens
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100.0%; Pred. No.
tive 0; Mismatc
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                                   US/09/041,889
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                                                                       Version #1.25
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5.8e-08;
                                                                                                                                                                                                                                   Suite 700
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US 08/837,058

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; MOLECULE TYPE: US-09-417-264-27
                Query Match
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/041,889
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-PM 3006
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27, Application US/09417264
Patent No. 6537768
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Ulgerative Colitis, and Treatment of
TITLE OF INVENTION: Microbial UC pANCA antigens
NUMBER OF SEQUENCES: 41
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.2
                                                                                                                                           TELEFAX: (619) 535-8949
                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acid
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,264
FILING DATE:
                                                                              TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
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APPLICATION NUMBER: US 0.
FILING DATE: 11-APR-1997
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                                                                                         amino acid
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California
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          40.1%;
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55.2%;
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     Score 58.5;
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Pred. No. 0.58;
2; Mismatches 10;
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     BG
   4.
Length 214;
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RESULT 14
US-09-270-767-55164
i Sequence 55164, Application US/09270767
i Patent No. 6703491
i GENERAL INFORMATION:
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US-09-270-767-39947
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Best Local :
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 39947
LENGTH: 93
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SEQ ID NO 7
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39947, Application US/09270767 Patent No. 6703491
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Best Local Similarity
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Matches 16, Conservative
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                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                  12;
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                                                                                                            AKTHQAAKKVLSPQDPRRQLTTMVAR 31
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                                                                                                                                                                               Conservative
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                                                                                                                                                                                           38.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.7%; Score 58; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.2%;
                                                                                                                                                                        Score 56; DB 4;
Pred. No. 0.55;
4; Mismatches ]
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2; Mismatches
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                                                                                                                                                                                                     Length 93;
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; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 55164
; SEQ ID NO 55164
; CURRENTH: 93
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-55164
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US-08-363-255-7
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                                                                                                                                US-08-363-255-7
                                                                                                                                                TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/363,255
FILING DATE: 23-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 25237-20002.22
TELEPHONE: (415) 813-5600
TELEPAN: (415) 494-0792
                                        Query Match 37.0%;
Best Local Similarity 44.4%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 38.4%; Score 56; DB 4; Length 93; Best Local Similarity 46.2%; Pred. No. 0.55; Matches 12; Conservative 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: JACOBS, Jr., WILLIAM R.

APPLICANT: BLOOM, BARRY R.

APPLICANT: COLLINS, DESMOND M.

APPLICANT: GELISLE, GEOFFREY W.

APPLICANT: MASCOPELLA, LISA

APPLICANT: KAWAKAMI, RIKU P.

TITLE OF INVENTION: MYCOBACTERIA VIRULENCE FACTORS AND A

TITLE OF INVENTION: MYCOBACTERIA VIRULENCE FACTORS AND A

TITLE OF INVENTION: MYCOBACTERIA VIRULENCE FACTORS AND A
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755 Page Mill Road
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                                        Score 54; DB 1;
Pred. No. 4.8;
2; Mismatches 1
                                          13; Indels
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Search completed: December 23, 2004, 11:35:52 Job time : 42 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2003as:*
6: geneseqp2003bs:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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   DB
   ADA13508
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Ada13508 Human H3
Ado21849 Human his
Abb07291 Human his
Abb07291 Histone 2
Aag07049 Arabidops
Aar46075 Histone H
Aag35461 Arabidops
Aag22671 Zea mays
Abp42906 Human ova
Aag13239 Arabidops
Aag91289 Human sec
Aag91289 Human sec
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Aag14100 Zea mays
Aag127142 Zea mays
Aag12241 Zea mays
Aag1252 Zea mays
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Aag12629 Zea mays
Aag1264980 Zea mays
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 20-FEB-2002; 2002US-0358325P
19-MAR-2002; 2002US-0365459P
                                                         19-FEB-2003; 2003WO-US004661
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Result

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ABB64138	ABB61842	AAM17089	AAG53099	AAG04323	AAG53145	AAG26219	AAG44415	AAG08768	AAG12084	AAG10324	AAG53143	AAG43813	AAG41099	AAG07917	AAG47930	AAG43664	ADE59334	AAY05483	AAY07285	
Abb64138	Abb61842	Aam17089	Aag53099	Aag04323	Aag53145	Aag26219	Aag44415	Aag08768	Aag12084	Aag10324	Aag53143	Aag43813	Aag41099	Aag07917	Aag47930	Aag43664	Ade59334	Aay05483	Aay07285	
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ALIGNMENTS

## Key Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Synthetic. detection; active gene; inactive gene; antibody; modified histone; tumour suppressor; oncogene; human; histone; epitope. Human H3 histone amino acid sequence. 20-NOV-2003 ADA13508 standard; peptide; 30 Modified-site Modified-site Homo sapiens. (first entry) /label= methylation 27 /label= acetylation 17 28 /label= phosphorylation Location/Qualifiers /label= methylation /label= acetylation 'label= acetylation /label= methylation 'label= phosphorylation label= acetylation or methylation label= methylation label= methylation ጅ

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RESULT 2
ADO21849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method for detecting active or inactive CC gene sequences in an individual. The method comprises: (a) contacting a cc body fluid sample with an antibody that binds to a modified histone CC associated with active or inactive gene sequences; (b) isolating cc the nucleosomes bound to the antibody; (c) purifying the DNA associated with CC Also described: (1) detecting active gene sequences in an individual, cc binds to a modified histone associated with an antibody that isolating nucleosomes bound to the antibody; (iii) purifying the DNA cc the purified DNA, (2) detecting inactive gene sequences in an individual, cc that in an individual, (2) detecting inactive gene sequences; (ii) contacting a body fluid sample with an antibody that contacting a body fluid sample with an antibody that comparising: (i) contacting inactive gene sequences; (ii) contacting a body fluid sample with an antibody that contacting a body fluid sample with an antibody that contacting a body fluid sample with an antibody that contacting a body fluid sample with an antibody that contacting a secutated with inactive gene sequences; (ii) associated with the nucleosomes is and (iv) identifying a gene encoded by the purified DNA; (3) isolating nucleosomes released from apoptotic cells of an individual; (4) detecting chromatin alterations associated with a cc in diagnosing a disease state such as inactivation of a tumour suppressor buman H3 histone amino acid sequence, which is given in the cc exemplification of the present invention.
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Best Local S
Matches 30
                               Modified-site
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                                                                                                                                                    Homo sapiens
                                                                                                                                                                     fusion protein reporter; histone modification; cytostatic; neuroprotective; muscular; virucide; cancer; neurological; muscular disorders; developmental; cell development; toxin toxic chemical; virus; human; histone H3; N-terminal.
                                                                                                                                                                                                                                                              Human histone H3 N-terminal peptide
                                                                                                                                                                                                                                                                                                          12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                      ADO21849 standard; peptide; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 30 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting active or inactive gene sequences associated with modified histones is useful to diagnose disease states, for example inactivation of a tumor suppressor gene or activation of an oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-697607/66
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"Post-translational modification
                                     "Post-translational
                                                                      "Post-translational
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                                                                                                                                                                                                                                                              ID 18).
                                 modification
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                                                                                                            RESULT 3
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     Human histone H3 protein amino
                                 02-APR-2002
                                                           ABB07291;
                                                                            ABB07291 standard; peptide;
                                                                                                                                                                                                                                                                      The invention relates to a novel fusion protein reporter comprising a core having a histone-modification-specific binding domain conjugated to a histone polypeptide, wherein the core is flanked by donor and acceptor fluorescent moieties. The molecules of the invention demonstrate useful for the diagnosis and/or treatment of histone modification disorders, such as cancer, neurological disorders, muscular addisorders, cell development disorders and disorders related to exposure to toxins, toxic chemicals or viruses. The
                                                                                                                                                                                                                                       Sequence 30 AA;
                                                                                                                                                                                                                                                     Current sequence is that of the human histone H3 N-terminal peptide ID 18) of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 15; SEQ ID NO 18; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                New fusion protein reporter having a core with a histone-modification-specific binding domain conjugated to a histone polypeptide, useful for diagnosing or treating cancer, viral infections, neurological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-420310/39
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05-AUG-2003; 2003US-00634740.
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Pred. No. 2.8e-13;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                      CENP-A antibody which specifically binds to phos CENP-A and coupled to a control of a coupled to coupled to the coupled to a coupled to the coupled to a coupled to detectable coupled to a coupled to coupled the coupled to a coupled to coupled to coupled the coupled to a coupled to coupled to coupled the coupled to coupled to coupled the coupled to coupled to coupled the coupled to coup
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel antibody directed against histone H3-like protein (CENP-A) that is phosphorylated at a specific position in the amino terminal part during mitosis in vivo, useful as marker of mitosis and in diagnostic imaging.
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 Human histone H3 N-terminal peptide (SEQ
                                    12-AUG-2004
                                                                                                                                                                                                                                                                                                                                Sequence 40
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                                                                                                      standard;
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Pred. No. 3.8e-13;
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                Histone 2A-derived gene delivery peptide #17
                                                    14-FEB-2002
                                                                                    AAU70897;
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(first entry)

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The invention relates to a novel fusion protein reporter comprising a core having a histone-modification-specific binding domain conjugated to a histone polypeptide, wherein the core is flanked by donor and acceptor fluorescent moieties. The molecules of the invention demonstrate cytostatic, neuroprotective, muscular and virucide activities and may be useful for the diagnosis and/or treatment of histone modification-ssociated disorders, such as cancer, neurological disorders muscular disorders, developmental disorders, cell development disorders and disorders related to exposure to toxins, toxic chemicals or viruses. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New fusion protein reporter having a core with a histone-modification-
specific binding domain conjugated to a histone polypeptide, useful for
diagnosing or treating cancer, viral infections, neurological and
muscular disorders.
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                                                                                                                                                                                         Sequence 40
                                                                                                                                                                                                                                                              current sequence is that of the human histone H3 N-terminal peptide
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05-AUG-2003;
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                                                                                                                                                                                                                                        invention.
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2003US-00634740.
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                                                                                         Score 146; DB o;
Pred. No. 3.8e-13;
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The invention relates to an isolated gene delivery facilitating peptide (CC (T) comprising at least 7 amino acids (preferably 17 amino acids) derived (T) comprising at least 7 amino acids (preferably 17 amino acids) derived (CC from the N-terminal region of Histone H2A, and which exhibits (CC for delivering a nucleic acid to cells. The gene delivery enhancing (CC peptide, derived from Histone H2A is complexed with a nucleic acid for CC peptide, derived from Histone H2A is complexed with a nucleic acid for CC principle that un-neutralised positive charges on the histone are bound (CC principle that un-neutralised positive charges on the histone are bound (CC principle that unclear targeting signals in the histones improve (CC trafficking of the DNA into the nucleus for transcription. This mode of (CC trafficking of the DNA into the nucleus for transcription. This mode of (CC trafficking viral and non-viral means, has minimum toxicity, with cellular (CC access, intracellular trafficking and nuclear retention of plasmids. The (CC access, intracellular trafficking and nuclear retention of plasmids. The (CC access, intracellular trafficking and muclear retention of plasmids. The (CC cound to mediate efficient delivery, providing an improved delivery of sequence. In addition, substitutions to the sequences have also been (CC system on the original H2A protein. AMU70877-AMU7093 represent histone (CC 2A-derived gene delivery peptides used in the method of the invention (CC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Histone H2A-derived peptides useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
(SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                          Sequence 55
                                                                                                                                                             AAG07049 standard; protein; 65 AA.
                                    protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 4051.
                                                                                                          17-OCT-2000 (first entry)
Arabidopsis thaliana
                           termination sequence.
                                                                                                                                                                                                                                                                                       1 Similarity
30; Conserv
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99US-0127462P

99US-013047PP

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99US-013048P

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99US-013942P

99US-0139458P

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RESULT 7
AAR46075
ID AAR46075;
XX AAR46075;
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05-OCT 1999
06-OCT 1999
07-OCT 1999
11-OCT 1999
  04-AUG-1992;
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19-OCT-1994
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                                                                                                                                                                                      sapiens.
                                                                                                                                                                                                                                     cDNA; library; enzyme;
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26-FEB-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA of human origin and proteins coded by it - which may be in vivo or in vitro translation using sense RNA or antisense corresponding to the cDNA.
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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
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06-AUG-1999; 99UE 06-AUG-1999; 99UE 09-AUG-1999; 99UE 10-AUG-1999; 99UE 11-AUG-1999; 99UE 12-AUG-1999; 99UE 13-AUG-1999; 99UE 13-AUG-1999; 99UE 13-AUG-1999; 99UE 13-AUG-1999; 99UE 13-AUG-1999; 99UE 13-AUG-1999; 99UE 23-AUG-1999; 99UE 23-AUG-1999; 99UE 23-AUG-1999; 99UE 23-AUG-1999; 99UE 25-AUG-1999; 99UE 27-AUG-1999;	27-JUL-1999; 99U 27-JUL-1999; 99U 27-JUL-1999; 99U 02-AUG-1999; 99U 02-AUG-1999; 99U 02-AUG-1999; 99U 03-AUG-1999; 99U 04-AUG-1999; 99U 04-AUG-1999; 99U 04-AUG-1999; 99U 04-AUG-1999; 99U 04-AUG-1999; 99U
06-AUG-1999; 99UE 06-AUG-1999; 99UE 09-AUG-1999; 99UE 10-AUG-1999; 99UE 11-AUG-1999; 99UE 12-AUG-1999; 99UE 13-AUG-1999; 99UE 13-AUG-1999; 99UE 13-AUG-1999; 99UE 13-AUG-1999; 99UE 13-AUG-1999; 99UE 13-AUG-1999; 99UE 23-AUG-1999; 99UE 23-AUG-1999; 99UE 23-AUG-1999; 99UE 23-AUG-1999; 99UE 25-AUG-1999; 99UE 27-AUG-1999;	27-JUL-1999; 99U 27-JUL-1999; 99U 27-JUL-1999; 99U 02-AUG-1999; 99U 02-AUG-1999; 99U 02-AUG-1999; 99U 03-AUG-1999; 99U 04-AUG-1999; 99U 04-AUG-1999; 99U 04-AUG-1999; 99U 04-AUG-1999; 99U 04-AUG-1999; 99U

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                 useful in cancer),
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26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                    The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABP4111-ABD55305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polymucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; uninary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis;
                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ov cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birse CE, Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-2000; 2000US-0209467P
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                                                                                                                                                                                                                                                                                                   Claim 11; SEQ ID NO 4038; 2922pp;
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99US-0161993P,
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Pred. No. 8.8e-13;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                   English.
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC disorders (e.g., infertility, disorders of pregnancy, anovulation, CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and CC vaginitis), immune disorders (e.g., congenital and acquired ophoritis and CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), CC inmunodericies, autoimmune oophoritis, systemic lupus erythematosus), CC and urinary disorders (e.g., anaemia), cardiovascular disorders, CC and urinary system disorders. Ovarian antigen polypeptides and CC polymucleotides may also be used in screening for compounds which CC modulate ovarian antigen expression or activity. The polymucleotides may further be used for gene therapy, chromosome mapping, in the CC identification of individuals and in forensic analysis, and the CC useful in disease diagnosis, drug targeting and phenotyping. The present CC sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO at figure and polymblished pct_sequences
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Best Local Similarity
25-PEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

01-APR-1999

01-APR-1999

16-APR-1999

16-APR-1999

21-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

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Pred. No. 9.1e-13;
); Mismatches 0;
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RESULT 12
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Best Local S
Matches 30
The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
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22-OCT-1999
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28-OCT-1999;
28-OCT-1999;
                                                                                                                                                                                                                     New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                             Claim 13; SEQ ID NO 5370; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                  N-PSDB; AAC01295.
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herapy; chromosome mapping.
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99US-0161406P
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Pred. No. 9.3e-13;
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RESULT 13
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Best Local Similarity
Matches: 30; Conserv
25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
23-MAR-1999
06-APR-1999
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21-MAY-1999
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31-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    termination sequence;
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99US-0130077P

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99US-013048P

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Query Match
Best Local
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11-AUG-1999
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 Score 146; DB 3;
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Mismatches 0;
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08-JUN-1999
10-JUN-1999
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110-JUN

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99US-013847P.
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Sequence 20, Application US/10258637

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| GENERAL INFORMATION:
| APPLICANT: Ballicki, Danuta |
| APPLICANT: Bealicki, Danuta |
| APPLICANTON: Histone H2A-derived peptides useful in gene delivery |
| FILE REFERENCE: TSRI 743.1 |
| CURRENT FILING DATE: 2001-04-24 |
| PRIOR APPLICATION NUMBER: PCT/EP01/04621 |
| PRIOR APPLICATION NUMBER: PCT/EP01/04621 |
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Publication No. US20040214272A1

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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Crou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NO 209506

SEQ ID NO 209506

LENGTH: 71
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NUMBER: Crouse Triangle Company Company Company
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US-10-424-599-282206
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US-10-425-115-238920
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US-10-425-115-238920
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Sequence 282206, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
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US-10-425-115-209506
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APPLICANT: LA ROSA, Thomas J.

APPLICANT: Caralic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21 (53222) B

CURRENT APPLICATION UNMERR: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 238920

LENGTH: 83
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Best Local !
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Best Local (
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LOCATION: (1)..(71)
OTHER INFORMATION: LEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 146; I ilarity 100.0%; Pred. No. 1. Conservative 0; Mismatches
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RESULT 6
US-10-425-115-218722
; Sequence 218722, Application US/10425115
; Publication No. US20040214272A1
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GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53222)B
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US-10-424-599-282206
                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
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SEQ ID NO 250033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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LENGTH: 85
TYPE: PRT
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TYPE: PRT
ORGANISM: Zea mays
FEATURE:
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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LOCATION: (1)..(85)
OTHER INFORMATION: unsure at all Xaa locations
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Pred. No. 1.7e-12;
Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR PILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR PILING DATE: 2000-06-07
PRIOR PILING DATE: 3.1
SEQ ID NO 4038
FENGTH: 93
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US-10-264-049-4038
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US-10-425-115-337375
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; OTHER INFORMATION: Clone ID: MRT4577_70856C.1.pep
US-10-425-115-337375
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; OTHER INFORMATION: Clone ID: MRT4577_131066C.1.pep
US-10-425-115-218722
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 337375
LENGTH: 90
TYPE: DEF
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 218722
LENGTH: 90
                                                                                                                                                                                                                                                                                                                     Sequence 4038, Application US/10264049 Publication No. US20040005579A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 30; Conservative 0
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Best Local
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APPLICANT: Kovallc, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                          APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA133P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Zea mays
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ORGANISM: Zea mays
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 100.0%; Score 146; DB 17; Local Similarity 100.0%; Pred. No. 1.8e-12;
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Pred. No. 1.8e-12;
D; Mismatches O;
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                                                                                                                                                                                                                                                                             and Antibodies
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; OTHER INFORMATION: Clone ID: MRT4577_70288C.1.pep
US-10-425-115-336777
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; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the twenty naturally US-10-264-049-4038
                                                                                                                                                                                                                                                                                           APPLICANT: La ROBA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules an
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-425-115-336777
                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 336777
LENGTH: 94
TYPE: PRT
ORGANIEM: Zea mays
                                                                     Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 336777, Application US/10425115
Publication No. US20040214272A1
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Best Local Similarity
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                     ARTKQTARKSTGGKAPRKQLATKAARKSAP 30
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ARTKOTARKSTGGKAPRKOLATKAARKSAP 36
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                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 146; DB 15; 100.0%; Pred. No. 1.9e-12;
                                                                     100.0%; Score 146; DB 17; 100.0%; Pred. No. 1.9e-12; tive 0; Mismatches 0;
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RESULT 10 US-10-425-115-223514 ; Sequence 223514, Application US/10425115

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RESULT 12
US-10-424-599-254928
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US-10-425-115-223514
                                                           Sequence 254928, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 250042
LENGTH: 109
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Best Local (
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Publication No. US20040214272A1
GENERAL INFORMATION:
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Best Local (
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LENGTH: 109
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)18
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: MRT4577_159622C.1.pep
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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Similarity 100.0%; Pred. No. 2.3e-12;
30; Conservative 0; Mismatches 0;
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US-10-425-115-333644, Application US/10425115; Sequence 333644, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:
; APPLICANT: La ROBA, Thomas J.
; APPLICANT: Kovalic, David K.
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US-10-425-115-368708
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US-10-424-599-254928
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Best Local S
Matches 30
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Publication No. US20040214272A1
GENERAL INFORMATION:
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SEQ ID NO 368708
LENGTH: 118
TYPE: PRT
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SEQ ID NO 254928
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
             APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
CURRENT APPLICATION NUMBER: US/10/425,115
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LOCATION: (1)..(117)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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ORGANISM: Glycine max
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 146; DB 17; llarity 100.0%; Pred. No. 2.4e-12; Conservative 0; Mismatches 0;
                                                               and Other Molecules Associated With
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The Park Lines

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APPLICANT: LA ROSS, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
CURRENT APPLICATION NUMBER: US/10/425,115:
CURRENT FILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 250032
LENGTH: 130
TYPE: PRT
ORGANIAM: Zea mays
PEATURE:
NAMB/KSY: unsure
LOCATION: (1)...(130)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_159613C.1.pep
US-10-425-115-250032
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US-10-425-115-250032

; Sequence 250032, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:
Search completed: December 23, 2004, 11:39:02 Job time : 150 secs
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                                                                                                                                                                           Query Match 100.0%; Score 146; DB 17; Best Local Similarity 100.0%; Pred. No. 2.7e-12; Matches 30; Conservative 0; Mismatches 0;
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NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 333644
LENGTH: 128
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LOCATION: (1)..(128)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Zea mays
FEATURE:
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                                                                                                                                                                                                                     Length 130;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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146
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74.013 Million cell updates/sec
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1: pir1:*
2: pir2:*
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4: pir4:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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100 /ative /TGGKA	hamster griseus squence len, S.; B7 pulatory s113; MU transla: M28265;	100. 100. 7ative 8TGGKAP	K 5 5 6 5 6		11366 11366 11366 11366 11366 11366
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imilarity 100.0%; Pred. No. 1. ; Conservative 0; Mismatches arTKQTARKSTGGKAPRKQLATKAARKSAP 30	744 a Da	imilarity 100.0%; Score 146; 100.0%; Pred. No. 1. 100.0%; Pred. No. 100.0%; Pred. No	e) ion 24 rratt, lation 249384	ALIGNMENTS	\$06743 149397 149398 1579198 561218 \$61218 \$61220 \$01120 \$01120 \$01197 \$01197 \$20669 \$20669 \$20669 \$301687 \$30
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R;Brandt, W.F.; Strikland, W.N.; Morgan, M.; Von Holt, C. FEBS Lett. 40, 167-172, 1974
A;Title: Comparison of the N-terminal amino acid sequences A;Accession: B61286; MUID:74299572; PMID:4851114
A;Accession: B61286
A;Status: preliminan
                                                                                                                                                                                                            nistone H3 - sandpaper limpet (fragment)
C;Species: Patella granatina (sandpaper limpet)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C;Accession: B61286
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R;Brandt, W.F.; Strickland, W.N.; Morgan, M.; Von Holt, C.
FEBS Lett. 40, 167-172, 1974
A;Title: Comparison of the N-terminal amino acid sequences
A;Reference number: A61286; MUID:74299572; PMID:4851114
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C;Species: Parechinus angulosus (angulate urchin)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change
C;Accession: A61286
                                                                               A; Molecule type: protein A; Residues: 1-48 < BRA>
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A;Title: Comparison of the N-terminal amino acid sequences
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C;Date: 19-Mar-1997 #sequence_revision
C;Accession: C61286
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                                                                 Cross-references: UNIPROT: Q7M3Z8
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histone H3.2 - alfalf
C;Species: Medicago s
C;Date: 14-Jun-1991 #
C;Accession: B38309
            J. Biol. Chem. 265, 17157-17161, 1990
A;Title: Sequence analysis of acetylation and methylation A;Reference number: A38309; MUID:91009145; PMID:2211618
A;Accession: A38309
A;Status: preliminary
A;Status: preliminary
                                                                                            A38309
A38309
Aistone H3.1 - alfalfa (fragments)
C;Species: Medicago sativa (alfalfa)
C;Date: 14-Jun-1991 #sequence_revision
C;Accession: A38309
C;Accession: A38309
C;Accession: A38309
C;Accession: A38309
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A;Molecule type: protein
A;Residues: 1-62 <WAT>
A;Cross-references: UNIPROT:P11105
C;Superfamily: histone H3
C;Keywords: chromosomal protein; Di
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A;Title: Sequence analysis of acetylation a
A;Reference number: A38309; MUID:91009145;
A;Accession: B38309
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submitted to the EMBL Data Library,
A;Reference number: S51664
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J. Biol. Chem. 26
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A; Residues: 1-60 < HAR>
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A,Molecule type: protein
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icago sativa (alfalfa)
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RESULT 9
A02630
histone H3 -
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A;Note: Cys-96 and Cys-110 can form an intrachain disulfide bond
A;Note: Lys-23 is acetylated in 43% of the molecules and Lys-14,
R;Pardridge, W.M.; Nowlin, D.M.; Calaycay, J.; Shively, J.E.
J. Neurochem. 53, 1014-1018, 1989
A;Title: Predominant low-molecular-weight proteins in isolated br
A;Reference number: PL0130; MUID:89361419; PMID:2769252
A;Accession: PL0130
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R;Goldberg, M.L.
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A;Cross-references: UN
C;Superfamily: histone
C;Keywords: chromosoma
R;Wakim, B.T., Aswad, G.D.
J. Biol. Chem. 269, 2722-2727, 1994
A;Title: Ca(2+)-calmodulin-dependent phosphorylation of arginine
A;Reference number: A49978; MUID:94132040; PMID:8300603
A;Accession: A49978
                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: A92132; MUID:73166574; PMID:4735580 A;Accession: A02624
                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Oct-1981 #sequence revision 08-Oct-1981 #text_change 09-Jul-2004
C;Accession: A02624; pt0130; A49978; S68319
C;Accession: A02624; Dt0130; A49978; S68319
R;DeLange, R.J.; Hooper, J.A.; Smith, E.L.
J. Biol. Chem. 248, 3261-3274, 1973
A;Title: Histone III. III. Sequence studies on the cyanogen bromide peptide
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C;Superfamily: histone H3
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A;Gene: FlyBase:His3
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A;Note: the author translated the
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A; Residues: 1-121 <GOL>
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;Species: Drosophila melanogaster
;Date: 31-Mar-1991 #sequence_revision 31-Mar-19;
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                                                                                                          Experimental source: brain
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Pred. No. 4.5e-12;
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A;Cross-references: UNIPROT:P08903
A;Experimental source: pollen
A;Note: 53-Uys, 96-Ser, 107-Ser, and 124-Val were also found
C;Superfamily: histone H3
C;Keywords: chromosomal protein; DNA binding; methylated amino acid; nucleosome cor
F;4/Modified site: N6-methyllysine or N6,N6-dimethyllysine (Lys) (partial) #status
F;9,27/Modified site: N6-methyllysine or N6,N6-dimethyllysine (Lys) #status experim
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R;Brandt, W.F.; von Holt, C.
FEBS Lett. 194, 278-281, 1986
A;Title: The primary structure
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C;Keywords: acetyllysine; chromosomal protein; DNA binding; methylated amino acid; nucl F;2.,128,139,131/Binding site: phosphate (Arg) (covalent) #status experimental F;2.,218,139,131/Binding site: N6-methyllysine, N6,N6-dimethyllysine or N6,N6-trimethyllysine F;9.,27/Modified site: N6-methyllysine, N6,N6-dimethyllysine or N6,N6,N6-trimethyllysine F;14,23/Binding site: acetyl (Lys) (covalent) (partial) #status experimental F;96,110/Disulfide bonds: interchain (in polymeric form) #status experimental F;96-110/Disulfide bonds: (in monomeric form) #status experimental
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A;Accession: A23604
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C/Species: Encephalartos altensteinii
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Arch. Biochem. Biophys. 325, 29-38, 1996
A;Title: Successive elution by ion-exchange chromatography of H3-H4 histone
A;Reference number: S68319; MUID:96140594; PMID:8554340
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J. Biol. Chem. 250, 1919-1920, 1975
A;Title: Histone III. IV. Two forms of calf thymus histone III.
A;Faterance number: A92174; MUID:75095680; PMID:1167550
A;Contents: annotation; variant
A;Note: analyses of two chymotryptic peptides, both corresponding
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A;Title: Histone III.
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J. Biol. Chem. 248, 3248-3254, 1973
A;Title: Histone III. I. Isolation
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R;Marzluff Jr., W.P.; Sanders, L.A.; Miller, D.M.; McCarty,
J. Biol. Chem. 247, 2026-2033, 1972
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Title: Histone III. II. Isolation and sequences of chymotryptic Reference number: A92131; MUID:73166573; PMID:4700459
Matches
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                                         100.0%; Score 146; DB 1 100.0%; Pred. No. 5e-12;
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histone H3 - striped catshark
C;Species: Poroderma africanum (striped catshark)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jt
C;Accession: A02626
R;Brandt, W.F.; Strickland, W.N.; von Holt, C.
FEBS Lett. 40, 349-352, 1974
A;Title: The primary structure of histone F3 from shark erythrocytes.
A;Reference number: A02626; MUID:74309063; PMID:4855011
A;Accession: A02626
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histone H3
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C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_
C;Accession: A02627
R;Hooper J.A.; Smith B.L.; Sommer, K.R.; Chalkley, R.
J. Biol. Chem. 248, 3275-3279, 1973
A;Title: Histone III. IV. Amino acid sequence of histone
A;Reference number: A02627; MUID:73166575; PMID:4700460
A;Accession: A02627
A;Molecule type: protein
A;Residues: 1-135 <HOO>
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A;Note: Lys-9 is epsilon-N-monomethyllysine, epsilon-N-dimethyllysine, epsilon-N-trimeth
A;Note: Lys-27 is epsilon-N-monomethyllysine, epsilon-N-dimethyllysine, epsilon-N-trimeth
C;Superfamily: histone H3
C;Keywords: chromosomal protein; DNA binding; methylated amino acid; nucleosome core
F;9,27/Modified site: N6-methyllysine, N6,N6-dimethyllysine or N6,N6,N6-trimethyllysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Patthy, L.; Smith, E.L.; Johnson, J.
J. Biol. Chem. 248, 6834-6840, 1973
A;Title: Histone III. V. The amino acid sequence of pea A;Reference number: A02631; MUID:74011270; PMID:4795661
A;Accession: A02631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: Lys-9 and Lys-27 are mainly epsilon-N-monomethyllysine. In a A;Note: 96-Ser was found in 40% of the molecules C;Superfamily: histone H3
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C;Species: Pisum sativum (garden pea)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
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;Species: Ictiobus bubalus (smallmouth buffalo fish)
;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
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100.0%; Pred. No. 5e-12;
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Search completed: December 23, Job time : 40 secs

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A;Note: Lys-9 (70%), Lys-27 (50%), and Lys-36 (20%) are methylated, mainly with the dimer of comment: The amount and position of acetylation was not precisely determined. Electrof c;Superfamily: histone H3 circumparts: chromosomal protein; DNA binding; methylated amino acid; nucle c;Superfamily: histone; chromosomal protein; DNA binding; methylated amino acid; nucle F;9,27,36/Modified site: N6-methyllysine or N6,N6-dimethyllysine (Lys) (partial) #status
                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-25 <CAN>
A;Residues: 1-25 <CAN>
C;Superfamily: histone H3
C;Keywords: acetyllysine; chromosomal protein; DNA binding; nucleosome core;
C;Keywords: acetyllysine; chromosomal protein; DNA binding; nucleosome core;
F;9,18/Binding site: acetyl (Lys) (covalent) (partial) #status experimental
F;14,23/Binding site: acetyl (Lys) (covalent) #status experimental
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A; Residues: 1-135 <BRA>
A; Cross-references: UNIPROT: P16105
A; Note: Lys-9 (70%), Lys-27 (50%),
A; Note: Lys-9 (70%), Lys-27 (50%),
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A;Molecule type: DNA
A;Residues: 1-135 <CON>
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tive 0; Mismatches
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